



ENTERED

13 2002

1638

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/026,400A

DATE: 02/25/2002

TIME: 13:42:15

Input Set : A:\2185-226.app

Output Set: N:\CRF3\02252002\I026400A.raw

3 <110> APPLICANT: MORI, Satoshi
4 NAKANISHI, Hiromi
5 TAKAHASHI, Michiko
7 <120> TITLE OF INVENTION: Nicotianamine Aminotransferase and Gene Therefor
9 <130> FILE REFERENCE: 2185-0226P
11 <140> CURRENT APPLICATION NUMBER: 09/026,400A
C--> 12 <141> CURRENT FILING DATE: 2002-01-31
14 <150> PRIOR APPLICATION NUMBER: 09-037499 JAPAN
15 <151> PRIOR FILING DATE: 1997-02-21
17 <160> NUMBER OF SEQ ID NOS: 7
19 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1660
23 <212> TYPE: DNA
24 <213> ORGANISM: Hordeum vulgare
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27 <221> NAME/KEY: CDS
28 <222> LOCATION: (62)..(1444)
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34 Met Val His Gln Ser Asn Gly His Gly Glu Ala Ala Ala Ala Ala Ala
35 1 5 10 15
37 aac ggc aag agc aac ggg cac gcc gcc gcc gcg aac ggc aag agc aac 157
38 Asn Gly Lys Ser Asn Gly His Ala Ala Ala Ala Asn Gly Lys Ser Asn
39 20 25 30
41 ggg cac gcg gcg gcg gcg gcg gtg gag tgg aat ttc gcc cgg ggc aag 205
42 Gly His Ala Ala Ala Ala Ala Val Glu Trp Asn Phe Ala Arg Gly Lys
43 35 40 45
45 gac ggc atc ctg gcg acg acg ggg gcg aag aac agc atc cgg gcg ata 253
46 Asp Gly Ile Leu Ala Thr Thr Gly Ala Lys Asn Ser Ile Arg Ala Ile
47 50 55 60
49 cgg tac aag atc agc gcg agc gtg gag gag agc ggg ccg cgg ccc gtg 301
50 Arg Tyr Lys Ile Ser Ala Ser Val Glu Glu Ser Gly Pro Arg Pro Val
51 65 70 75 80
53 ctg ccg ctg gcc cac ggt gac ccg tcc gtg ttc ccg gcc ttc cgc acg 349
54 Leu Pro Leu Ala His Gly Asp Pro Ser Val Phe Pro Ala Phe Arg Thr
55 85 90 95
57 gcc gtc gag gcc gaa gac gcc gtc gcc gcc gcg ctg cgc acc ggc cag 397
58 Ala Val Glu Ala Glu Asp Ala Val Ala Ala Leu Arg Thr Gly Gln
59 100 105 110
61 ttc aac tgc tac gcc gcc ggc gtc ggc ctc ccc gcc gca cga agc gcc 445
62 Phe Asn Cys Tyr Ala Ala Gly Val Gly Leu Pro Ala Ala Arg Ser Ala

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63	115	120	125	
65	gta gca gag cac ttg tca cag ggc gtg ccc tac aag cta tcg gcc gac	493		
66	Val Ala Glu His Leu Ser Gln Gly Val Pro Tyr Lys Leu Ser Ala Asp			
67	130	135	140	
69	gac gtc ttc ctc acc gcc ggc gga act cag gcg atc gaa gtc ata atc	541		
70	Asp Val Phe Leu Thr Ala Gly Gly Thr Gln Ala Ile Glu Val Ile Ile			
71	145	150	155	160
73	ccg gtg ctg gcc cag act gcc ggc gcc aac ata ctg ctt ccc cgg cca	589		
74	Pro Val Leu Ala Gln Thr Ala Gly Ala Asn Ile Leu Leu Pro Arg Pro			
75	165	170	175	
77	ggc tat cca aat tac gag gcg cga gcg gca ttc aac aag ctg gag gtc	637		
78	Gly Tyr Pro Asn Tyr Glu Ala Arg Ala Ala Phe Asn Lys Leu Glu Val			
79	180	185	190	
81	cgg cac ttc gac ctc atc ccc gac aag ggg tgg gag atc gac atc gac	685		
82	Arg His Phe Asp Leu Ile Pro Asp Lys Gly Trp Glu Ile Asp Ile Asp			
83	195	200	205	
85	tcg ctg gaa tcc atc gcc gac aag aac acc acc gcg atg gtc atc ata	733		
86	Ser Leu Glu Ser Ile Ala Asp Lys Asn Thr Thr Ala Met Val Ile Ile			
87	210	215	220	
89	aac cca aac aat ccg tgc ggc agc gtt tac tcc tac gac cat ctg gcc	781		
90	Asn Pro Asn Asn Pro Cys Gly Ser Val Tyr Ser Tyr Asp His Leu Ala			
91	225	230	235	240
93	aag gtc gcg gag gtg gca agg aag ctc gga ata ttg gtg atc gct gac	829		
94	Lys Val Ala Glu Val Ala Arg Lys Leu Gly Ile Leu Val Ile Ala Asp			
95	245	250	255	
97	gag gtt tac ggc aaa ctg gtt ctg ggc agc gcc ccg ttt atc ccg atg	877		
98	Glu Val Tyr Gly Lys Leu Val Leu Gly Ser Ala Pro Phe Ile Pro Met			
99	260	265	270	
101	ggc gtc ttt ggg cac att gcc ccg gtc ttg tcc att gga tct ctg tcc	925		
102	Gly Val Phe Gly His Ile Ala Pro Val Leu Ser Ile Gly Ser Leu Ser			
103	275	280	285	
105	aag tcg tgg ata gtg cct gga tgg cga ctt gga tgg gtg gcg gtg tac	973		
106	Lys Ser Trp Ile Val Pro Gly Trp Arg Leu Gly Trp Val Ala Val Tyr			
107	290	295	300	
109	gac ccc aca aag att tta gag aaa act aag atc tct acg tct att acg	1021		
110	Asp Pro Thr Lys Ile Leu Glu Lys Thr Lys Ile Ser Thr Ser Ile Thr			
111	305	310	315	320
113	aat tac ctt aat gtc tca acg gac cca gca acc ttc gtt cag gaa gct	1069		
114	Asn Tyr Leu Asn Val Ser Thr Asp Pro Ala Thr Phe Val Gln Glu Ala			
115	325	330	335	
117	ctt cct aaa att ctt gag aac aca aaa gca gat ttc ttt aag agg att	1117		
118	Leu Pro Lys Ile Leu Glu Asn Thr Lys Ala Asp Phe Phe Lys Arg Ile			
119	340	345	350	
121	att ggt cta aag gaa tca tca gag ata tgt tat agg gaa ata aag	1165		
122	Ile Gly Leu Lys Glu Ser Ser Glu Ile Cys Tyr Arg Glu Ile Lys			
123	355	360	365	
125	gaa aac aaa tat att acg tgt cct cac aag cca gaa gga tcg atg ttt	1213		
126	Glu Asn Lys Tyr Ile Thr Cys Pro His Lys Pro Glu Gly Ser Met Phe			
127	370	375	380	

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129 gta atg gtc aaa cta aac tta cat ctt ttg gag gag atc cat gac gac 1261
130 Val Met Val Lys Leu Asn Leu His Leu Leu Glu Glu Ile His Asp Asp
131 385 390 395 400
133 ata gat ttt tgc tgc aag ctc gca aag gaa gaa tca gta att tta tgt 1309
134 Ile Asp Phe Cys Cys Lys Leu Ala Lys Glu Glu Ser Val Ile Leu Cys
135 405 410 415
137 cca ggg agt gtt ctt gga atg gaa aat tgg gtc cgt att act ttt gcc 1357
138 Pro Gly Ser Val Leu Gly Met Glu Asn Trp Val Arg Ile Thr Phe Ala
139 420 425 430
141 tgc gtt cca tct tct ctt caa gat gga ctc gaa agg gtc aaa tca ttc 1405
142 Cys Val Pro Ser Ser Leu Gln Asp Gly Leu Glu Arg Val Lys Ser Phe
143 435 440 445
145 tgt caa agg aac aag aag aag aat tct ata aat ggt tgt tagttgtaca 1454
146 Cys Gln Arg Asn Lys Lys Lys Asn Ser Ile Asn Gly Cys
147 450 455 460
149 caccctagt tgtacatctg actgaagctg taaatcattt ctagttatcc cccatttata 1514
151 tatttcaata aaacatattg taatggttct gttgtagctg tccaagtcac gtactctact 1574
153 ttttgatgta tttggcctca ttgccttgca tcaatttcaa taaaaatggt tgtgtacacc 1634
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159 <211> LENGTH: 461
160 <212> TYPE: PRT
161 <213> ORGANISM: Hordeum vulgare
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170 Gly His Ala Ala Ala Ala Ala Val Glu Trp Asn Phe Ala Arg Gly Lys
171 35 40 45
173 Asp Gly Ile Leu Ala Thr Thr Gly Ala Lys Asn Ser Ile Arg Ala Ile
174 50 55 60
176 Arg Tyr Lys Ile Ser Ala Ser Val Glu Glu Ser Gly Pro Arg Pro Val
177 65 70 75 80
179 Leu Pro Leu Ala His Gly Asp Pro Ser Val Phe Pro Ala Phe Arg Thr
180 85 90 95
182 Ala Val Glu Ala Glu Asp Ala Val Ala Ala Ala Leu Arg Thr Gly Gln
183 100 105 110
185 Phe Asn Cys Tyr Ala Ala Gly Val Gly Leu Pro Ala Ala Arg Ser Ala
186 115 120 125
188 Val Ala Glu His Leu Ser Gln Gly Val Pro Tyr Lys Leu Ser Ala Asp
189 130 135 140
191 Asp Val Phe Leu Thr Ala Gly Gly Thr Gln Ala Ile Glu Val Ile Ile
192 145 150 155 160
194 Pro Val Leu Ala Gln Thr Ala Gly Ala Asn Ile Leu Leu Pro Arg Pro
195 165 170 175
197 Gly Tyr Pro Asn Tyr Glu Ala Arg Ala Ala Phe Asn Lys Leu Glu Val
198 180 185 190
200 Arg His Phe Asp Leu Ile Pro Asp Lys Gly Trp Glu Ile Asp Ile Asp
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206 Asn Pro Asn Asn Pro Cys Gly Ser Val Tyr Ser Tyr Asp His Leu Ala
207 225          230          235          240
209 Lys Val Ala Glu Val Ala Arg Lys Leu Gly Ile Leu Val Ile Ala Asp
210          245          250          255
212 Glu Val Tyr Gly Lys Leu Val Leu Gly Ser Ala Pro Phe Ile Pro Met
213          260          265          270
215 Gly Val Phe Gly His Ile Ala Pro Val Leu Ser Ile Gly Ser Leu Ser
216          275          280          285
218 Lys Ser Trp Ile Val Pro Gly Trp Arg Leu Gly Trp Val Ala Val Tyr
219          290          295          300
221 Asp Pro Thr Lys Ile Leu Glu Lys Thr Lys Ile Ser Thr Ser Ile Thr
222 305          310          315          320
224 Asn Tyr Leu Asn Val Ser Thr Asp Pro Ala Thr Phe Val Gln Glu Ala
225          325          330          335
227 Leu Pro Lys Ile Leu Glu Asn Thr Lys Ala Asp Phe Phe Lys Arg Ile
228          340          345          350
230 Ile Gly Leu Leu Lys Glu Ser Ser Glu Ile Cys Tyr Arg Glu Ile Lys
231          355          360          365
233 Glu Asn Lys Tyr Ile Thr Cys Pro His Lys Pro Glu Gly Ser Met Phe
234          370          375          380
236 Val Met Val Lys Leu Asn Leu His Leu Leu Glu Glu Ile His Asp Asp
237 385          390          395          400
239 Ile Asp Phe Cys Cys Lys Leu Ala Lys Glu Glu Ser Val Ile Leu Cys
240          405          410          415
242 Pro Gly Ser Val Leu Gly Met Glu Asn Trp Val Arg Ile Thr Phe Ala
243          420          425          430
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254 <212> TYPE: DNA
255 <213> ORGANISM: Hordeum vulgare
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258 <221> NAME/KEY: CDS
259 <222> LOCATION: (76)..(1728)
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265          Met Ala Thr Val Arg Gln Ser Asp Gly Val Ala Ala
266          1          5          10
268 aac ggc ott gcc gtg gcc gca gcc gcg aac ggc aag agc aac ggc cat 159
269 Asn Gly Leu Ala Val Ala Ala Ala Asn Gly Lys Ser Asn Gly His
270          15          20          25
272 ggc gtg gct gcc gcc gtg aac ggc aag agc aac ggc cat ggc gtg gat 207

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273	Gly	Val	Ala	Ala	Ala	Val	Asn	Gly	Lys	Ser	Asn	Gly	His	Gly	Val	Asp	
274		30					35					40					
276	gcc	gac	gcg	aac	ggc	aag	agc	aac	ggc	cat	ggc	gtg	gct	gcc	gac	gcg	255
277	Ala	Asp	Ala	Asn	Gly	Lys	Ser	Asn	Gly	His	Gly	Val	Ala	Ala	Asp	Ala	
278	45					50					55					60	
280	aac	ggc	aag	agc	aac	ggc	cat	gcc	gag	gcc	act	gcg	aac	ggc	cac	ggc	303
281	Asn	Gly	Lys	Ser	Asn	Gly	His	Ala	Glu	Ala	Thr	Ala	Asn	Gly	His	Gly	
282					65					70					75		
284	gag	gcc	act	gcg	aac	ggc	aag	acc	aac	ggc	cac	cgc	gag	agc	aac	ggc	351
285	Glu	Ala	Thr	Ala	Asn	Gly	Lys	Thr	Asn	Gly	His	Arg	Glu	Ser	Asn	Gly	
286				80					85						90		
288	cat	gct	gag	gcc	gcc	gac	gcg	aac	ggc	gag	agc	aac	gag	cat	gcc	gag	399
289	His	Ala	Glu	Ala	Ala	Asp	Ala	Asn	Gly	Glu	Ser	Asn	Glu	His	Ala	Glu	
290			95					100					105				
292	gac	tcc	gcg	gcg	aac	ggc	gag	agc	aac	ggg	cat	gcg	gcg	gcg	gcg	gca	447
293	Asp	Ser	Ala	Ala	Asn	Gly	Glu	Ser	Asn	Gly	His	Ala	Ala	Ala	Ala	Ala	
294	110					115						120					
296	gag	gag	gag	gag	gcg	gtg	gag	tgg	aat	ttc	gcg	ggt	gcc	aag	gac	ggc	495
297	Glu	Glu	Glu	Glu	Ala	Val	Glu	Trp	Asn	Phe	Ala	Gly	Ala	Lys	Asp	Gly	
298	125				130						135					140	
300	gtg	ctg	gcg	gcg	acg	ggg	gcg	aac	atg	agc	atc	cgg	gcg	ata	cgg	tac	543
301	Val	Leu	Ala	Ala	Thr	Gly	Ala	Asn	Met	Ser	Ile	Arg	Ala	Ile	Arg	Tyr	
302				145					150						155		
304	aag	atc	agc	gcg	agc	gtg	cag	gag	aag	ggg	ccg	cgg	ccc	gtg	ctg	ccg	591
305	Lys	Ile	Ser	Ala	Ser	Val	Gln	Glu	Lys	Gly	Pro	Arg	Pro	Val	Leu	Pro	
306				160					165					170			
308	ctg	gcc	cac	ggg	gac	ccg	tcc	gtg	ttc	ccg	gcc	ttc	cgc	acg	gcc	gtc	639
309	Leu	Ala	His	Gly	Asp	Pro	Ser	Val	Phe	Pro	Ala	Phe	Arg	Thr	Ala	Val	
310			175					180					185				
312	gag	gcc	gag	gac	gcc	gtc	gcc	gcc	gcc	gtg	cgc	acc	ggc	cag	ttc	aac	687
313	Glu	Ala	Glu	Asp	Ala	Val	Ala	Ala	Ala	Val	Arg	Thr	Gly	Gln	Phe	Asn	
314	190					195					200						
316	tgc	tac	ccc	gcc	ggc	gtc	ggc	ctc	ccc	gcc	gca	cga	agc	gcc	gtg	gca	735
317	Cys	Tyr	Pro	Ala	Gly	Val	Gly	Leu	Pro	Ala	Ala	Arg	Ser	Ala	Val	Ala	
318	205					210					215					220	
320	gag	cac	ctg	tcg	cag	ggc	gtg	ccg	tac	atg	cta	tcg	gcc	gac	gac	gtc	783
321	Glu	His	Leu	Ser	Gln	Gly	Val	Pro	Tyr	Met	Leu	Ser	Ala	Asp	Asp	Val	
322				225					230					235			
324	ttc	ctc	acc	gcc	ggc	ggg	acc	cag	gcg	atc	gag	gtc	ata	atc	ccg	gtg	831
325	Phe	Leu	Thr	Ala	Gly	Gly	Thr	Gln	Ala	Ile	Glu	Val	Ile	Ile	Pro	Val	
326			240						245					250			
328	ctg	gcc	cag	acc	gcc	ggc	gcc	aac	att	ctg	ctc	ccc	agg	cca	ggc	tac	879
329	Leu	Ala	Gln	Thr	Ala	Gly	Ala	Asn	Ile	Leu	Leu	Pro	Arg	Pro	Gly	Tyr	
330			255					260						265			
332	cca	aac	tac	gag	gcg	cgc	gcc	gcg	ttc	aac	agg	ctg	gag	gtc	cgg	cat	927
333	Pro	Asn	Tyr	Glu	Ala	Arg	Ala	Ala	Phe	Asn	Arg	Leu	Glu	Val	Arg	His	
334	270					275						280					
336	ttc	gac	ctc	atc	ccc	gac	aag	ggg	tgg	gag	atc	gac	atc	gac	tcg	ctg	975
337	Phe	Asp	Leu	Ile	Pro	Asp	Lys	Gly	Trp	Glu	Ile	Asp	Ile	Asp	Ser	Leu	

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\2185-226.app

Output Set: N:\CRF3\02252002\I026400A.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:537 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:554 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6